

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hawkins, Phillip R.  
Murry, Lynn E.

(ii) TITLE OF THE INVENTION: HUMAN PHOSPHOLIPASE INHIBITOR

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: U.S.  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Filed Herewith

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Luther, Barbara J.  
(B) REGISTRATION NUMBER: 33,954  
(C) REFERENCE/DOCKET NUMBER: PF-0059-1 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1LPB02  
(B) CLONE: CONSENSUS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

NCAATGGGCC GGCGTGGGA AGGGTGAATG TGGGTCCAGA CCCGCCCTC CTCAGCTTCC

60

TATAAAAGCT	GGGGACCAGG	TACTGCTGAT	ACACACACCA	TGAGGCTCTC	CAGGAGACCA	120
GAGACCTTTC	TGCTGGCCTT	TGTGTTGCTC	TGCACCCCTCC	TGGGTCTTGG	GTGCCCACTA	180
CACTGCGAAA	TATGTACGGC	GGCGGGGAGC	AGGTGCCATG	GCCAAATGAA	GACCTGCAGC	240
AGTGACAAGG	ACACATGTGT	GCTCCTGGTC	GGGAAGGCTA	CTTCAAAGGG	CAAGGAGTTG	300
GTGCACACCT	ACAAGGGCTG	CATCAGGTCC	CAGGACTGCT	ACTCCGGCGT	TATATCCACC	360
ACCATGGGCC	CCAAGGACCA	CATGGTAACC	AGCTCCTTCT	GCTGCCAGAG	CGACGGCTGC	420
AACAGTGCTC	TTTTGTCTGT	TCCCTTGACC	AATCTTACTG	AGAATGGCCT	GATGTGCC	480
GCCTGCACTG	CGAGCTTCAG	GGACAAATGC	ATGGGGCCCA	TGACCCACTG	TACTGGAAAG	540
GAAAACCACT	GCGTCTCCTT	ATCTGGACAC	GTGCAGGCTG	GTATTTCAA	ACCCAGATT	600
GCTATGCGGG	GCTGTGCTAC	AGAGAGTATG	TGCTTTACCA	AGCCTGGTGC	TGAAGTACCC	660
ACAGGCACCA	ATGTCCTCTT	CCTCCATCAT	ATAGAGTGCA	CTCACTCCCC	CTGAAAAGCT	720
ATCTGAACAG	AGGAAGATAA	TGTAGTGTGA	AGTC	CTGACTTC	CTGTAAC	780
CCC GTGTGCC	TATAAGAAG	TTAATAGAGC	AAAAAAA	AAAAAAA	AAACTCGAG	839

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: CONSENSUS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Leu Ser Arg Arg Pro Glu Thr Phe Leu Leu Ala Phe Val Leu  
 1                   5                   10                   15  
 Leu Cys Thr Leu Leu Gly Leu Gly Cys Pro Leu His Cys Glu Ile Cys  
 20               25               30  
 Thr Ala Ala Gly Ser Arg Cys His Gly Gln Met Lys Thr Cys Ser Ser  
 35               40               45  
 Asp Lys Asp Thr Cys Val Leu Leu Val Gly Lys Ala Thr Ser Lys Gly  
 50               55               60  
 Lys Glu Leu Val His Thr Tyr Lys Gly Cys Ile Arg Ser Gln Asp Cys  
 65               70               75               80  
 Tyr Ser Gly Val Ile Ser Thr Thr Met Gly Pro Lys Asp His Met Val  
 85               90               95  
 Thr Ser Ser Phe Cys Cys Gln Ser Asp Gly Cys Asn Ser Ala Phe Leu  
 100              105              110  
 Ser Val Pro Leu Thr Asn Leu Thr Glu Asn Gly Leu Met Cys Pro Ala  
 115              120              125  
 Cys Thr Ala Ser Phe Arg Asp Lys Cys Met Gly Pro Met Thr His Cys  
 130              135              140  
 Thr Gly Lys Glu Asn His Cys Val Ser Leu Ser Gly His Val Gln Ala  
 145              150              155              160  
 Gly Ile Phe Lys Pro Arg Phe Ala Met Arg Gly Cys Ala Thr Glu Ser  
 165              170              175  
 Met Cys Phe Thr Lys Pro Gly Ala Glu Val Pro Thr Gly Thr Asn Val  
 180              185              190  
 Leu Phe Leu His His Ile Glu Cys Thr His Ser Pro  
 195              200

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: GI 501050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Tyr Leu His Thr Ile Cys Leu Leu Phe Ile Phe Val Ala Arg  
1 5 10 15  
Gly Asn Ser Arg Ser Cys Asp Phe Cys His Asn Ile Gly Lys Asp Cys  
20 25 30  
Asp Gly Tyr Glu Glu Cys Ser Ser Pro Glu Asp Val Cys Gly Lys  
35 40 45  
Val Leu Leu Glu Ile Ser Ser Ala Ser Leu Ser Val Arg Thr Val His  
50 55 60  
Lys Asn Cys Phe Ser Ser Ser Ile Cys Lys Leu Gly Gln Phe Asp Val  
65 70 75 80  
Asn Ile Gly His His Ser Tyr Ile Arg Gly Arg Ile Asn Cys Cys Glu  
85 90 95  
Lys Glu Leu Cys Glu Asp Gln Pro Phe Pro Gly Leu Pro Leu Ser Lys  
100 105 110  
Pro Asn Gly Tyr Tyr Cys Pro Gly Ala Ile Gly Leu Phe Thr Lys Asp  
115 120 125  
Ser Thr Glu Tyr Glu Ala Ile Cys Lys Gly Thr Glu Thr Lys Cys Ile  
130 135 140  
Asn Ile Val Gly His Arg Tyr Glu Gln Phe Pro Gly Asp Ile Ser Tyr  
145 150 155 160  
Asn Leu Lys Gly Cys Val Ser Ser Cys Pro Leu Leu Ser Leu Ser Asn  
165 170 175  
Ala Thr Phe Glu Gln Asn Arg Asn Tyr Leu Glu Lys Val Glu Cys Lys  
180 185 190  
Asp Ala Ile Arg Leu Ala Ser Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

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(A) LIBRARY: HMC1N0T01  
(B) CLONE: 8941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAGGCCTAG	GGTTAGGCAA	GACCTTGAGG	CAGGGGTTGA	AGCCAGGGAG	TGGTCAGCCA	60
GCACTGTCCC	TGCCGTCCC	CATCCCACAG	AGGGCAAGGA	GTTGGTGCAC	ACCTACAAGG	120
GCTGCATCAG	GTCCCAGGAC	TGCTACTCG	GCGTTATATC	NACCACCATG	GGCCCCAAGG	180
ACCACATGGT	AACCAGCTCC	TTCTGNTGCC	AGAGCGACGG	CTGCAACAGT	GCCTTTTGT	240
CTGTTCCCTT	GACCAATCTT	ACTGAGAATG	GCCTGATGTG	CCCNGCTGCA	CTGCGAGTTT	300
NAGGGNAAA	ATNCATGGGG	GCCCATT				327

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 324 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: THP1LPB01  
(B) CLONE: 10033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTGCTCTNC	ACCCCTCCTGG	GTCTGGGTG	CCCACTACAC	TGCGAAATAT	GTACGGCGGC	60
GGGGAGCAGG	TGCCATGGCC	AAATGAAGAC	CTGCAGCAGT	GACAAGGACA	CATGTGTGCT	120
CCTGGTCGGG	AAGGCTACTT	CAAAGGGCAA	GGAGTTGGTG	CACACCTACA	AGGGCTGCAT	180
CAGGTCCCGAG	GACTGCTACT	CCGGCGTTAT	ATCCACCACC	ATGGGCCCCA	AGGACCACAT	240
GGTAACCAGC	TCCTTCTGCT	GCAGAGCGAC	GGCTGCAACA	GTGCCTTTT	GTCTGTTCCC	300
TTGACCAATC	TTACTGAGAA	TGGT				324

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: THP1LPB01  
(B) CLONE: 10644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACACATGTG	TNCTCCTGGT	CGGGAAGGCT	ACTTCAAAGG	GCAAGGAGTT	GGTGCACACC	60
TACAAGGGCT	GCATCAGGTN	CCAGGACTGC	TACTCCGGNG	TTATATCCAC	CACCATGGGC	120
CCCAAGGACC	ACATGGTAAC	CAGCTCCTTC	TGCTGCCAGA	GCGACGGCTG	CAACAGTGCC	180

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TTTTTGTCTG TTCCCTTGAC CAATNTTACT GAGAATNGNC TGATGTGCCCGNCTGCACT	240
GNGAGCTTCA GGGACAAATG CT	262

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1LPB01  
(B) CLONE: 10774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACACATGTG TGCTCCTGGT CGGGAAGGCT ACTTCAAAGG GCAAGGAGTT GGTGCACACC	60
TACAAGGGCT GCATCAGGTC CCAGGACTGC TACTCCGGNG TTATATCCAC CACCATGGGC	120
CCCAAGGACC ACATGGTAAC CAGCTCCTTC TGCTGCCAGA GCGACGGCTG CAACAGTGCC	180
TTTTTGTCTG TTCCCTTANC CAATCTTACT GAGAATGGCC TGATGTGCCCGNCTGAAC	240
NCGAGCTTCA GGGACAAATN CATGGGNNA TGACCCACTG TACTGGNAAG NNAAACCACT	300
GNNGTGTCCCTT	310

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1PEB01  
(B) CLONE: 71854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCCGGCGTT ATATCCACCA CCATGGGCC CAAGGACAC ATGGTAACCA GCTCCTTCTG	60
CTGCCAGAGC GACGGCTGCA ACANTGCCTT TTTNTNTGTT CCCTTGACCA ATCTTACTGA	120
GAATGGCCTG ATGTGCCCG CCTGCACTGC GAGCTTCAGG GACAAATGCA TGGGGCCCAT	180
GACCC	185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: THP1PEB01
  - (B) CLONE: 72861
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTGGTGCAC ACCTACAAGG GCTGCATCAAG GTCCCAAGGAC TTCTACTCCG GNGTTATATC	60
CACCACCATG GGCCCCAAGG ACCACATGGT AACCAAGCTCC TTNTGCTGCC AGAGCGACGG	120
CTGCAACATT GCCTTTTTNT NTGTNCCCTT G	151

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 144 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: THP1PEB01
  - (B) CLONE: 74452
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGACTGCT ACTCCGGNGT TATATCCACC ACCATGGGCC CCAAGGACCA CATGGTAACC	60
AGCTCCTTCT GCTGCCAGAG CNACGGCTGC AACANTGCCT TTNTGTCTGT NCCCTTGACC	120
AATCTNACTG AGAATNGCCT GATT	144

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 174 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: THP1LPB02
  - (B) CLONE: 155045
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CNTGGCCTTA GTTTNCNCT CACCCTCCNG GGTCTNGGGT GCCCACNACA CTGCGAANTA	60
TGTACGGCGG CGGGTAGCAG GTTCCATGNC CAAATNAAGA NCTTCANCNG TGACAAGGAC	120
ACATGTNTGC TCCTGGTCGG NAAGNCTACT TCAAAGGGCA AGGAGTTGGT GCAC	174

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1LPB02
- (B) CLONE: 156817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTGGCCTTTG	TGTTGCTCTG	CACCCTCCTG	GGTCTTGGGT	GCCCAC TACA	CTGC GAAATA	60
TGTACGGCGG	CGGGGAGCAG	GTGCCATGGC	CAAATGAAGA	CCTGCAGCAG	TGACAAGGAC	120
ACATGTGTGC	TCCTGGTCGG	GAAGGCTACT	TCAAAGGGCA	AGGAGTTNGT	GCACACCTAC	180
AAGGGCTGCA	TCAT					194

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PGANNOT01
- (B) CLONE: 619856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAAGAGAC	CATNCCAGGA	AGTTGTGGGG	TTGGGGAGGC	CTAGGGTTAG	GCAAGACCTT	60
GAGGCAGGGG	TTGAAGCCAG	GGAGTGGTCA	GCCAGCACTG	TCCCTGCCCTG	TCCCCATCCC	120
ACAGAGGGCA	AGGAGTTGGT	GCACA ACTAC	AAGGGCTGCA	TCAGGTCCCA	GGACTGCTAC	180
TNCGGNGTTA	TATCCACCAAC	CATGGGCC	AAGGACCACA	TGGT		224

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSN0T02

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(B) CLONE: 683480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTGGTGCAC ACCTACAAGG GCTGCATCAG GTCCCAGGAC TGCTACTCCG GCGTTATATN	60
CACCACCATG GGNCCAAGG ACCACATGGT AACCAAGCTCC TTNTGCTGCC AGAGCGACGN	120
CTGCAACAGT GCCTTTTGT CTGTTCCCTT GACCAATCTT ACTGAGAATG GCCTGATGTG	180
CCCCGNCTGC ACTGCGAGCT TNAGGGACAA ATGCATGGGG CCCATGACCC ACTGTACTGG	240
AGAGGAAAAC CA	252

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT11
- (B) CLONE: 1291208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

GGGAATCCCA GTTCTTGCAG CCACTGGAA TCAAGAGGCC CAACTCCGTC TTGGTCTTNN	60
NNNNNNNNNN NNNNNNNCAA TGGGCCGGCC GTGGGAAGGG TGAATGTGGG TCCAGACCCG	120
CCCCCTCCTCA GCTTCCTATA AAAGCTGGGG ACCAGGTACT GCTGATACAC ACACCATGAG	180
GCTCTCCAGG AGACCAGAGA CCTTTCTGCT GGCCCTTGTG TTGCTCTGCA CCCTCCTGGG	240
TCTTGGGTGC	250